In the Claims:

Kindly cancel claims 1-19, 21 and 23 add new claims 35-47 and enter the following proposed amendments to claims 20, 22, 24-33:

20. A method for analyzing a nucleic acid sample comprising:

fragmenting the nucleic acid sample using a first and second restriction enzyme to produce fragments;

ligating adaptors to the fragments;

amplifying the fragments, wherein fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme are enriched in the amplification product relative to the fragments that were cut on both ends by the same restriction enzyme;

providing a nucleic acid array consisting essentially of probes designed to detect the alleles present at polymorphisms predicted to be present on fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

hybridizing the amplified fragments to the array; and

analyzing a hybridization pattern resulting from the hybridization.

22. The method of claim 20 wherein the polymorphisms are single nucleotide polymorphisms (SNPs).

24. The method of claim 20 wherein polymorphisms predicted to be present on fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme are first determined by a computer system.

25. A method of determining the alleles present at a polymorphism in an individual comprising:

providing a nucleic acid sample from the individual;

fragmenting the nucleic acid sample using a first and second restriction enzyme to produce fragments wherein the polymorphism is predicted to be on a

fragment that was cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating adaptors to the fragments; and

amplifying the fragments, wherein fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme are predominant in the amplification product relative to the fragments that were cut on both ends by the same restriction enzyme;

providing a nucleic acid array consisting essentially of probes to determine the alleles present at polymorphisms predicted to be present on fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

hybridizing the amplified fragments to the array;

generating a hybridization pattern resulting from the hybridization; and

determining the alleles present at the polymorphism in the individual based upon an analysis of the hybridization pattern.

26. The method of claim 25 wherein the polymorphism is a single nucleotide polymorphism (SNP).

27. The method of claim 26 wherein the SNP is associated with a disease.

28. The method of claim 26 wherein the SNP is associated with the efficacy of a drug.

29. A method of determining the alleles present at a single nucleotide polymorphism in a population of individuals comprising:

providing a first nucleic acid sample from each of the individuals;

providing a second nucleic acid sample by:

fragmenting the nucleic acid sample using a first and second restriction enzyme to produce fragments wherein the polymorphism is predicted to be

on a fragment that was cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating adaptors to the fragments; and

amplifying the fragments, wherein fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme are predominant in the amplification product relative to the fragments that were cut on both ends by the same restriction enzyme;

providing a plurality of identical nucleic acid arrays wherein the arrays consist essentially of probes to determine the alleles present at polymorphisms predicted to be present on fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

hybridizing each of the second nucleic acid samples to one of the plurality of identical arrays;

generating a plurality of hybridization patterns resulting from the hybridizations; and

analyzing the hybridization patterns to determine the alleles present at the polymorphism in the population of individuals.

30. The method of claim 29 wherein the polymorphism is a single nucleotide polymorphism (SNP).

31. The method of claim 30 wherein the SNP is associated with a disease.

32: The method of claim 30 wherein the SNP is associated with the efficacy of a drug.

33. A method of genotyping an individual comprising:

providing a first nucleic acid sample from the individual;

providing a second nucleic acid sample by:

fragmenting the nucleic acid sample using a first and second restriction enzyme to produce fragments wherein a collection of polymorphisms is

predicted to be present on fragments cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating adaptors to the fragments; and

amplifying the fragments, wherein fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme are predominant in the amplification product relative to the fragments that were cut on both ends by the same restriction enzyme;

hybridizing the second nucleic acid sample to an array designed to determine the presence or absence of one or more alleles of one or more polymorphisms present in the collection of polymorphisms;

generating a hybridization pattern resulting from the hybridizations; and

determining the presence or absence of the one or more alleles of one or more polymorphisms present in the collection of polymorphisms.

35. (New) The method of claim 20 wherein the fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 0.01% of the first nucleic acid sample.

36. (New) The method of claim 20 wherein the fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 0.5% of the first nucleic acid sample.

37. (New) The method of claim 20 wherein the fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 3% of the first nucleic acid sample.

38. (New) The method of claim 20 wherein the fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 12% of the first nucleic acid sample.

39. (New) The method of claim 20 wherein the fragments that were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 30% of the first nucleic acid sample.

40. (New) The method of claim 20 wherein the nucleic acid sample is genomic DNA, DNA, or double stranded cDNA derived from RNA, total RNA or mRNA.

41. (New) The method of claim 20 wherein ligation of one strand of each adaptor to the fragments is blocked.

42. (New) The method of claim 41 wherein ligation is blocked by introducing a gap of at least one nucleotide between one strand of the adaptor and one strand of the fragment.

43. (New) The method of claim 41 wherein ligation is blocked by the absence of a phosphate at the 5' end of an adaptor strand.

44. (New) The method of claim 41 wherein ligation is blocked by the presence of a modified nucleotide at the 5' or 3' end of an adaptor strand.

45. (New) The method of claim 41 wherein ligation is blocked by a terminal modification in one strand of an adaptor.

46. (New) The method of claim 41 wherein ligation is blocked at the 5' end of one strand of one adaptor and at the 3' end of one strand of the other adaptor.

47. (New) The method of claim 41 wherein ligation is blocked at the 5' end of both strands of one adaptor and at the 3' end of both strands of the other adaptor.